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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2012; month=1; day=27; hr=9; min=13; sec=58; ms=415;]

=====

Reviewer Comments:

<210> 70

<211> 174

<212> PRT

<213> Oerskovia jenensis

<400> 70

(ERRORED PORTION SHOWN BELOW)

Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala

115

120

125

Please remove the blank lines between the above amino acid numbers and their respective amino acids; amino acid numbers must appear directly below their respective amino acids.

<210> 134

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 134

(ERRORED PORTION SHOWN BELOW)

Val Asn Glu Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His

50

55

60

Please remove the blank lines between the above amino acid numbers and their respective amino acids; amino acid numbers must appear directly below their amino acids.

<210> 639
<211> 255
<212> PRT
<213> Streptogrisin C

Regarding the above "<213>" response: Reminder: per 1.823 of the Sequence Rules, the only valid "<213>" responses are: the Genus species of the organism, "Artificial Sequence", or "Unknown". "Artificial Sequence" and "Unknown" require explanation in the "<220>--<223>" section: please clearly indicate the source of the genetic material. "Streptogrisin" also appears in the "<213>" response in subsequent sequences.

<210> 640
<211> 185
<212> PRT
<213> Streptogrisin B

<400> 640

(please see below)

Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu
1 5 10 15
Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly

20

25

30

"Streptogrisin" appears in the above "<213>" response. Also, please remove the blank lines between the above amino acid numbers and their amino acids.

<210> 642

<211> 188

<212> PRT

<213> Streptogrisin D

<400> 642

(please see below)

Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val His Asp Gly

100

105

110

"Streptogrisin" appears in the above "<213>" response. Also, please remove the blank lines between the above amino acid numbers and their amino acids.

To correct the sequence listing errors noted in this report - The recommended method for correction of errors is to access the sequence listing working file using the software program in which the listing was originally prepared, e.g., the project file in PatentIn, make any necessary corrections within that program, then generate a new sequence listing file. Use of a word processing program to correct errors directly in the original sequence listing file is strongly discouraged, since such programs often introduce unintended changes to the sequence listing, rendering the listing unacceptable. When the working file or original program is not available for correction, then use of a common or plain text-only editor, such as NotePad, to edit the original sequence listing file may suffice.

Application No: 10576331 Version No: 3.0

Input Set:

Output Set:

Started: 2012-01-26 20:11:11.447
Finished: 2012-01-26 20:11:31.273
Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 826 ms
Total Warnings: 605
Total Errors: 28
No. of SeqIDs Defined: 656
Actual SeqID Count: 656

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 251	Found intentionally skipped sequence in SEQID (18)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 402	Undefined organism found in <213> in SEQ ID (38)

Input Set:

Output Set:

Started: 2012-01-26 20:11:11.447
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No. of SeqIDs Defined: 656
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Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (45)
W 213	Artificial or Unknown found in <213> in SEQ ID (46)
W 213	Artificial or Unknown found in <213> in SEQ ID (47)
W 213	Artificial or Unknown found in <213> in SEQ ID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (49)
W 213	Artificial or Unknown found in <213> in SEQ ID (50)
W 213	Artificial or Unknown found in <213> in SEQ ID (51)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
W 402	Undefined organism found in <213> in SEQ ID (61)
W 402	Undefined organism found in <213> in SEQ ID (62)
W 402	Undefined organism found in <213> in SEQ ID (65)
W 402	Undefined organism found in <213> in SEQ ID (66)
W 402	Undefined organism found in <213> in SEQ ID (69)
W 402	Undefined organism found in <213> in SEQ ID (70) This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (70)
W 213	Artificial or Unknown found in <213> in SEQ ID (79)
W 213	Artificial or Unknown found in <213> in SEQ ID (80)
W 213	Artificial or Unknown found in <213> in SEQ ID (81)
W 213	Artificial or Unknown found in <213> in SEQ ID (82)
W 213	Artificial or Unknown found in <213> in SEQ ID (83)

Input Set:

Output Set:

Started: 2012-01-26 20:11:11.447
Finished: 2012-01-26 20:11:31.273
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Total Warnings: 605
Total Errors: 28
No. of SeqIDs Defined: 656
Actual SeqID Count: 656

Error code	Error Description		
W 213	Artificial or Unknown found in <213>	in SEQ ID (84)	
	This error has occurred more than 20 times, will not be displayed		
E 341	'Xaa' position not defined	SEQID (125)	POS (170)
E 341	'Xaa' position not defined	SEQID (125)	POS (171)
E 341	'Xaa' position not defined	SEQID (125)	POS (172)
E 341	'Xaa' position not defined	SEQID (125)	POS (173)
E 341	'Xaa' position not defined	SEQID (125)	POS (174)
E 341	'Xaa' position not defined	SEQID (125)	POS (175)
E 341	'Xaa' position not defined	SEQID (125)	POS (176)
E 341	'Xaa' position not defined	SEQID (125)	POS (177)
E 341	'Xaa' position not defined	SEQID (125)	POS (178)
E 341	'Xaa' position not defined	SEQID (125)	POS (179)
E 341	'Xaa' position not defined	SEQID (125)	POS (180)
E 341	'Xaa' position not defined	SEQID (125)	POS (181)
E 341	'Xaa' position not defined	SEQID (125)	POS (182)
E 341	'Xaa' position not defined	SEQID (125)	POS (183)
E 341	'Xaa' position not defined	SEQID (125)	POS (184)
E 341	'Xaa' position not defined	SEQID (125)	POS (185)
E 341	'Xaa' position not defined	SEQID (125)	POS (186)
E 341	'Xaa' position not defined	SEQID (125)	POS (187)
E 341	'Xaa' position not defined	SEQID (125)	POS (188)
E 341	'Xaa' position not defined	SEQID (125)	POS (189)
	This error has occurred more than 20 times, will not be displayed		

Input Set:

Output Set:

Started: 2012-01-26 20:11:11.447
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Total Warnings: 605
Total Errors: 28
No. of SeqIDs Defined: 656
Actual SeqID Count: 656

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (134)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (640)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (642)

SEQUENCE LISTING

<110> Jones, Brian E.
Kolkman, Marc
Leefflang, Chris
Oh, Hiroshi
Poulose, A.J.
Sadlowski, Eugene S.
Shaw, Andrew
van der Kleij, Wilhelmus A.H.
van Marrenwijk, Leo

<120> Serine Proteases, Nucleic Acids Encoding Serine Enzymes and
Vectors and Host Cells Incorporating Same

<130> GC819-2-US/B

<140> 10576331
<141> 2012-01-26

<150> PCT/US2004/039066
<151> 2004-11-19

<150> US 60/523,609
<151> 2003-11-19

<160> 656

<170> PatentIn version 3.2

<210> 1
<211> 1680
<212> DNA
<213> Cellulomonas strain 69B4

<400> 1

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accagcacgc	tcctaaccctc	cgagcacccgg	cgaccggcg	gtgcgtatgaa	agggacgaaac	180
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cgacctctac	gtgcagcgct	ggaacggcag	ctccctgggt	accgtcgccc	agagcaccc	1560
ccccggctcc	aacgagacca	tcacctaccc	cggcaacgccc	ggctactacc	gctacgtgg	1620
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<210> 2

<211> 1488

<212> DNA

<213> Cellulomonas strain 69B4

<400> 2

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ccacgcctgg	ccgagaagct	cgaccccgac	ctctcgagg	ccatggagcg	cgacccctggc	180
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ctgtacgtcg	ccaccaccga	cgaggacgc	gtcgaggagg	tcgagggcga	aggcgccacg	360
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ggctccaacg	agaccatcac	ctaccgcggc	aacgcccgt	actaccgcta	cgtggtaaac	1440
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<210> 3

<211> 1404

<212> DNA

<213> Cellulomonas spp.

<400> 3

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accctggcgt	tccagcacga	cgcagccgag	accggcgagg	ccctcgccga	agagctcgac	180
gaggacttcg	ccggcacctg	ggtcgaggac	gacgtctgt	acgtcgccac	caccgacgag	240
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gtcgagaccc	acgagacccc	gcccggat	ttcgacgtga	tcggcggcaa	cgcctacacc	540
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ggccactgcg	gccgcacccgg	cgtccaccacc	gccaacccca	ccgggacctt	cgccgggtcc	660
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<210> 4
<211> 567
<212> DNA
<213> Cellulomonas spp.

<400> 4	tcggccgcaa	cgcctacacc	atcgaaaaaa	gcagccgctg	ctcgatcgaa	60
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gccaacccca	ccgggacctt	cggccgggtcc	agttcccg	gcaacgacta	cgcgttcgtc	180
cgtaccgggg	ccggcgtgaa	cctgctggcc	caggtcaaca	actactccgg	tggccgggtc	240
caggtcgccg	ggcacaccgc	ggcccccgtc	ggctcgccgg	tgtccgggtc	cgggtcgacc	300
accgggtggc	actgcggcac	catcaactcct	cggtcaccta	ccccgagggc		360
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ggtggcacca	cgttcttcca	gccggtaaac	ccatcctcc	aggcgtaacgg	cctgaggatg	540
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<210> 5
<211> 83
<212> DNA
<213> Cellulomonas strain 69B4

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<210> 6
<211> 495
<212> PRT
<213> Cellulomonas strain 69B4

<400> 6

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							20				25		30		
Pro	Pro	Gly	Ser	Ala	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Glu	Lys	Leu	Asp
							35			40		45			
Pro	Asp	Leu	Leu	Glu	Ala	Met	Glu	Arg	Asp	Leu	Gly	Leu	Asp	Ala	Glu
						50			55		60				
Glu	Ala	Ala	Ala	Thr	Leu	Ala	Phe	Gln	His	Asp	Ala	Ala	Glu	Thr	Gly

65	70	75	80
Glu Ala Leu Ala Glu	Glu Leu Asp	Glu Phe Ala Gly	Thr Trp Val
85	90	95	
Glu Asp Asp Val	Leu Tyr Val Ala Thr	Thr Asp Glu Asp Ala Val	Glu
100	105	110	
Glu Val Glu Gly	Glu Gly Ala Thr	Ala Val Thr Val	Glu His Ser Leu
115	120	125	
Ala Asp Leu Glu Ala	Trp Lys Thr Val	Leu Asp Ala Ala	Leu Glu Gly
130	135	140	
His Asp Asp Val Pro	Thr Trp Tyr Val Asp	Val Pro Thr Asn Ser	Val
145	150	155	160
Val Val Ala Val Lys	Ala Gly Ala Gln	Asp Val Ala Ala	Gly Leu Val
165	170	175	
Glu Gly Ala Asp Val Pro	Ser Asp Ala Val	Thr Phe Val	Glu Thr Asp
180	185	190	
Glu Thr Pro Arg Thr	Met Phe Asp Val	Ile Gly Gly	Asn Ala Tyr Thr
195	200	205	
Ile Gly Gly Arg Ser	Arg Cys Ser Ile	Gly Phe Ala Val	Asn Gly Gly
210	215	220	
Phe Ile Thr Ala Gly	His Cys Gly Arg	Thr Gly Ala	Thr Thr Ala Asn
225	230	235	240
Pro Thr Gly Thr Phe	Ala Gly Ser Ser	Phe Pro Gly Asn	Asp Tyr Ala
245	250	255	
Phe Val Arg Thr Gly	Ala Gly Val Asn	Leu Ala Gln Val	Asn Asn
260	265	270	
Tyr Ser Gly Gly Arg	Val Gln Val	Ala Gly His	Thr Ala Ala Pro Val
275	280	285	
Gly Ser Ala Val Cys	Arg Ser Gly Ser	Thr Thr Gly	Trp His Cys Gly
290	295	300	
Thr Ile Thr Ala Leu	Asn Ser Ser Val	Thr Tyr Pro	Glu Gly Thr Val
305	310	315	320
Arg Gly Leu Ile Arg	Thr Thr Val Cys	Ala Glu Pro	Gly Asp Ser Gly
325	330	335	
Gly Ser Leu Leu Ala	Gly Asn Gln	Ala Gln Gly Val	Thr Ser Gly Gly
340	345	350	
Ser Gly Asn Cys	Arg Thr Gly	Thr Phe Phe	Gln Pro Val Asn
355	360	365	
Pro Ile Leu Gln Ala	Tyr Gly Leu Arg	Met Ile Thr	Thr Asp Ser Gly
370	375	380	
Ser Ser Pro Ala Pro	Ala Pro Thr Ser	Cys Thr Gly	Tyr Ala Arg Thr
385	390	395	400
Phe Thr Gly Thr Leu	Ala Ala Gly Arg	Ala Ala Gln Pro	Asn Gly
405	410	415	
Ser Tyr Val Gln Val	Asn Arg Ser Gly	Thr His Ser Val	Cys Leu Asn
420	425	430	
Gly Pro Ser Gly Ala Asp	Phe Asp Leu	Tyr Val Gln	Arg Trp Asn Gly
435	440	445	
Ser Ser Trp Val Thr	Val Ala Gln	Ser Thr Ser	Pro Gly Ser Asn Glu
450	455	460	
Thr Ile Thr Tyr Arg	Gly Asn Ala	Gly Tyr Tyr	Arg Tyr Val Val Asn
465	470	475	480
Ala Ala Ser Gly Ser	Gly Ala Tyr	Thr Met Gly	Leu Thr Leu Pro
485	490	495	

<210> 7
<211> 467
<212> PRT

<213> Cellulomonas strain 69B4

<400> 7

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20 25 30
Leu Asp Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala
35 40 45
Ala Glu Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala
50 55 60
Gly Thr Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu
65 70 75 80
Asp Ala Val Glu Val Glu Gly Glu Ala Thr Ala Val Thr Val
85 90 95
Glu His Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala
100 105 110
Ala Leu Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro
115 120 125
Thr Asn Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala
130 135 140
Ala Gly Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe
145 150 155 160
Val Glu Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly
165 170 175
Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala
180 185 190
Val Asn Gly Gly Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala
195 200 205
Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly
210 215 220
Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
225 230 235 240
Gln Val Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr
245 250 255
Ala Ala Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly
260 265 270
Trp His Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro
275 280 285
Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro
290 295 300
Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val
305 310 315 320
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe
325 330 335
Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr
340 345 350
Thr Asp Ser Gly Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly
355 360 365
Tyr Ala Arg Thr Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala
370 375 380
Gln Pro Asn Gly Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser
385 390 395 400
Val Cys Leu Asn Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln
405 410 415
Arg Trp Asn Gly Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro

420 425 430
Gly Ser Asn Glu Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg
435 440 445
Tyr Val Val Asn Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu
450 455 460
Thr Leu Pro
465

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<212> PRT
<213> Cellulomonas strain 69B4

<400> 8

Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg
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Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
20 25 30
Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
35 40 45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
50 55 60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
65 70 75 80
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
85 90 95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
100 105 110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
115 120 125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
130 135 140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145 150 155 160
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
165 170 175
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
180 185

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<212> PRT
<213> Cellulomonas strain 69B4

<400> 9

Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
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Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
20 25

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<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t
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23

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